```
(1) GENERAL INFORMATION:
   5
            (i) APPLICANT: Anderson, Dirk M.
                           Galibert, Laurent
                           Maraskovsky, Eugene
 10
           (ii) TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
          (iii) NUMBER OF SEQUENCES: 19
           (iv) CORRESPONDENCE ADDRESS:
 15
                 (A) ADDRESSEE: Immunex Corporation, Law Department
                 (B) STREET: 51 University Street
                 (C) CITY: Seattle
                 (D) STATE: WA
                 (E) COUNTRY: USA
 20
                 (F) ZIP: 98101
           (v) COMPUTER READABLE FORM:
                 (A) MEDIUM TYPE: Floppy disk
                 (B) COMPUTER: Apple Power Macintosh
 25
                (C) OPERATING SYSTEM: Apple Operating System 7.5.5
                (D) SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
         (vi) CURRENT APPLICATION DATA:
                (A) APPLICATION NUMBER:
 30
                (B) FILING DATE: 22 DECEMBER 1997
                (C) CLASSIFICATION:
         (vii) PRIOR APPLICATION DATA:
                (A) APPLICATION NUMBER: USSN 60/064,671
35
                (B) FILING DATE: 14 OCTOBER 1997
                (C) CLASSIFICATION:
         (vii) PRIOR APPLICATION DATA:
                (A) APPLICATION NUMBER: USSN 08/813,509
40
                (B) FILING DATE: 07 MARCH 1997
                (C) CLASSIFICATION:
         (vii) PRIOR APPLICATION DATA:
                (A) APPLICATION NUMBER: USSN 08/772,330 (60/064,671)
45
                (B) FILING DATE: 23 DECEMBER 1996
                (C) CLASSIFICATION:
       (viii) ATTORNEY/AGENT INFORMATION:
                (A) NAME: Perkins, Patricia Anne
50
                (B) REGISTRATION NUMBER: 34,693
                (C) REFERENCE/DOCKET NUMBER: 2852-A
         (ix) TELECOMMUNICATION INFORMATION:
                (A) TELEPHONE: (206)587-0430
55
               (B) TELEFAX: (206)233-0644
     (2) INFORMATION FOR SEQ ID NO:1:
60
         (i) SEQUENCE CHARACTERISTICS:
```



Docket No. 2852-A

	IMMUNEX CORPORATION	
5	<ul><li>(A) LENGTH: 3115 base</li><li>(B) TYPE: nucleic aci</li><li>(C) STRANDEDNESS: sin</li><li>(D) TOPOLOGY: linear</li></ul>	ď
	(ii) MOLECULE TYPE: cDNA	
	(iii) HYPOTHETICAL: NO	
10	(iv) ANTI-SENSE: NO	

### (A) ORGANISM: HOMO SAPIENS 15 (vii) IMMEDIATE SOURCE:

(vi) ORIGINAL SOURCE:

(A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS

(B) CLONE: 9D-8A

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 93..1868

25	(xi)	SEQUENCE	DESCRIPTION:	SEQ	ID	NO:1:
23						

20												,						
	GCT	GCTG	CTG	CTCT	GCGC	GC I	GCTC	GCCC	G GC	TGCA	GTTI	r TAT	CCAC	AAA	GAGC	TGTGTG		60
30	GAC	TCTC	TGC	CTGA	CCTC	'AG T	GTTC	<b>TT</b> T	Ç AG	GTG Val 1	Ala	TTC Lev	G CAG	ATC Ile	Ala	CCT Pro	1	13
35	CCA Pro	TGT Cys	ACC Thr 10	Ser	GAG Glu	AAG Lys	CAT His	тат Туг 15	Glu	CAT His	CTG Leu	GGA Gly	CGG Arg 20	Cys	TGT Cys	AAC Asn	1	.61
	AAA Lys	TGT Cys 25	GAA Glu	CCA Pro	GGA Gly	AAG Lys	ТАС Туг 30	ATG Met	TCT Ser	TCT Ser	AAA Lys	TGC Cys 35	ACT Thr	ACT Thr	ACC Thr	TCT Ser	2	09
40	GAC Asp 40	Ser	GTA Val	TGT Cys	CTG Leu	CCC Pro 45	TGT Cys	GGC Gly	CCG Pro	GAT Asp	GAA Glu 50	TAC Tyr	TTG Leu	GAT Asp	AGC Ser	TGG Trp 55	2	57
45	AAT Asn	GAA Glu	GAA Glu	GAT Asp	AAA Lys 60	TGC Cys	TTG Leu	CTG Leu	CAT His	AAA Lys 65	GTT Val	TGT Cys	GAT Asp	ACA Thr	GGC Gly 70	AAG Lys	3	05
50	GCC Ala	CTG Leu	GTG Val	GCC Ala 75	GTG Val	GTC Val	GCC Ala	GGC Gly	AAC Asn 80	AGC Ser	ACG Thr	ACC Thr	CCC Pro	CGG Arg 85	CGC Arg	TGC Cys	3	53
55	GCG Ala	TGC Cys	ACG Thr 90	GCT Ala	GGG Gly	TAC Tyr	CAC His	TGG Trp 95	AGC Ser	CAG Gln	GAC Asp	TGC Cys	GAG Glu 100	TGC Cys	TGC Cys	CGC Arg	40	01
	CGC Arg	AAC Asn 105	ACC Thr	GAG Glu	TGC Cys	GCG Ala	CCG Pro 110	GGC Gly	CTG Leu	GGC Gly	GCC Ala	CAG Gln 115	CAC His	CCG Pro	TTG Leu	CAG Gln	44	49

	IM	MUN	EX CO	ORPO	RATIO	NC										Docke	t No. 2852-A
	CTC Let 120	u As	C AA( n Ly:	G GA( s Ası	C ACA	A GTG Val 125	l Cys	C AAA	A CC' s Pro	T TG	C CT s Le 13	u Al	A GG a Gl	С ТА У Ту	C TT	C TCT e Ser 135	407
5	GA: Ası	r GC o Al	C TT a Phe	T TCC	TCC Ser 140	Thi	GAC Asp	AAA Lys	A TGO	C AG S Are	g Pr	C TG o Tr	G AC p Th	C AA r As	C TG n Cy 15	T ACC s Thr	545
10	TT( Phe	C CT	r GGA u Gly	A AAC / Lys 155	Arg	GTA Val	GAA Glu	CAT His	CAT His	Gl	G AC	A GAG	G AA u Ly	A TC s Se 16	r Ası	r GCG o Ala	593
15	GT7 Val	TGC Cys	C AGT S Ser 170	Ser	TCT Ser	CTG Leu	CCA Pro	GCT Ala 175	Arg	AAA Lys	A CC	A CCA	A AA' O Asi 180	n Gl	A CCC	C CAT O His	641
20	GTT Val	ТА( Тул 185	Leu	CCC Pro	GGT Gly	TTA Leu	ATA Ile 190	ATT Ile	CTG Leu	CTI Leu	CTC Let	TTC Phe 195	e Ala	G TC:	r GTC	GCC Ala	689
	CTG Leu 200	val	GCT Ala	GCC Ala	ATC Ile	ATC Ile 205	TTT Phe	GGC Gly	GTT Val	TGC Cys	TAT Tyr 210	Arg	AA. Lys	A AAA 6 Lys	GGG Gly	AAA Lys 215	737
25	GCA Ala	CTC Leu	ACA Thr	GCT Ala	AAT Asn 220	TTG Leu	TGG Trp	CAC His	TGG Trp	ATC Ile 225	Asn	GAG	GCT Ala	TG1 Cys	GGC Gly 230	CGC Arg	785
30	CTA Leu	AGT Ser	GGA Gly	GAT Asp 235	AAG Lys	GAG Glu	TCC Ser	TCA Ser	GGT Gly 240	GAC Asp	AGT Ser	TGT Cys	GTC Val	AGT Ser 245	Thr	CAC His	833
35	ACG Thr	GCA Ala	AAC Asn 250	TTT Phe	GGT Gly	CAG Gln	CAG Gln	GGA Gly 255	GCA Ala	TGT Cys	GAA Glu	GGT Gly	GTC Val 260	TTA Leu	CTG Leu	CTG Leu	881
40	ACT Thr	CTG Leu 265	GAG Glu	GAG Glu	AAG Lys	ACA Thr	TTT Phe 270	CCA Pro	GAA Glu	GAT Asp	ATG Met	TGC Cys 275	TAC Tyr	CCA Pro	GAT Asp	CAA Gln	929
	GGT Gly 280	GGT Gly	GTC Val	TGT Cys	CAG Gln	GGC Gly 285	ACG Thr	TGT Cys	GTA Val	GGA Gly	GGT Gly 290	GGT Gly	CCC Pro	TAC Tyr	GCA Ala	CAA Gln 295	977
45	GGC Gly	GAA Glu	GAT Asp	GCC Ala	AGG Arg 300	ATG Met	CTC Leu	TCA Ser	TTG Leu	GTC Val 305	AGC Ser	AAG Lys	ACC Thr	GAG Glu	ATA Ile 310	GAG Glu	1025
50	GAA Glu	GAC Asp	AGC Ser	TTC Phe 315	AGA Arg	CAG Gln	ATG Met	Pro '	ACA Thr 320	GAA Glu	GAT Asp	GAA Glu	TAC Tyr	ATG Met 325	GAC Asp	AGG Arg	1073
55	CCC Pro	TCC Ser	CAG Gln 330	CCC Pro	ACA (	GAC ( Asp (	Gln :	TTA ( Leu :	CTG Leu	TTC Phe	CTC Leu	ACT Thr	GAG Glu 340	CCT Pro	GGA Gly	AGC Ser	1121
60	Lys	TCC Ser 345	ACA Thr	CCT Pro	CCT (	Phe :	PCT ( Ser ( 350	GAA ( Glu 1	CCC ( Pro :	CTG Leu	Glu	GTG Val 355	GGG Gly	GAG Glu	AAT Asn	GAC Asp	1169

	IMMUNEX CORPORATION  AGT TTA AGC CAG TGC TTC ACG GGG ACA CAG AGC ACA GTG GGT TCA GAA													No. 2852-A			
	AGT Ser 360	Leu	AGC Ser	CAG Gln	TGC Cys	TTC Phe 365	Thr	Gly	ACA Thi	A CAG	G AGC Ser 370	Thi	GTC Val	G GGT Gly	TCA Ser	GAA Glu 375	1217
5	AGC Ser	TGC Cys	AAC Asn	TGC Cys	ACT Thr 380	Glu	CCC Pro	CTG Leu	TGC Cys	AGG Arg 385	Thi	GAT Asp	TGC Trp	ACT Thr	CCC Pro	ATG Met	1265
10	TCC Ser	TCT Ser	GAA Glu	AAC Asn 395	Tyr	TTG Leu	CAA Gln	AAA Lys	GAG Glu 400	\Val	GAC Asp	: AGT Ser	GGC Gly	CAT His 405	TGC Cys	CCG Pro	1313
15	CAC His	TGG Trp	GCA Ala 410	GCC Ala	AGC Ser	CCC Pro	AGC Ser	CCC Pro 415	Asn	TGG Trp	GCA Ala	GAT Asp	GTC Val 420		ACA Thr	GGC Gly	1361
20	TGC Cys	CGG Arg 425	AAC Asn	CCT Pro	CCT Pro	GGG Gly	GAG Glu 430	GAC Asp	TGT Cys	GAA Glu	CCC Pro	CTC Leu 435	Val	GGT Gly	TCC Ser	CCA Pro	1409
	AAA Lys 440	CGT Arg	GGA Gly	CCC Pro	TTG Leu	CCC Pro 445	CAG Gln	TGC Cys	GCC Ala	TAT Tyr	GGC Gly 450	ATG Met	GGC	CTT Leu	CCC Pro	CCT Pro 455	1457
25	GAA Glu	GAA Glu	GAA Glu	GCC Ala	AGC Ser 460	AGG Arg	ACG Thr	GAG Glu	GCC Ala	AGA Arg 465	GAC Asp	CAG Gln	CCC Pro	GAG Glu	GAT Asp 470	GGG Gly	1505
30	GCT Ala	GAT Asp	GGG Gly	AGG Arg 475	CTC Leu	CCA Pro	AGC Ser	TCA Ser	GCG Ala 480	AGG Arg	GCA Ala	GGT Gly	GCC Ala	GGG Gly 485	TCT Ser	GGA Gly	1553
35	AGC Ser	TCC Ser	CCT Pro 490	GGT Gly	GGC Gly	CAG Gln	TCC Ser	CCT Pro 495	GCA Ala	TCT Ser	GGA Gly	AAT Asn	GTG Val 500	ACT Thr	GGA Gly	AAC Asn	1601
40	AGT Ser	AAC Asn 505	TCC Ser	ACG Thr	TTC Phe	ATC Ile	TCC Ser 510	AGC Ser	GGG Gly	CAG Gln	GTG Val	ATG Met 515	AAC Asn	TTC Phe	AAG Lys	GGC Gly	1649
	GAC Asp 520	ATC Ile	ATC Ile	GTG Val	GTC Val	TAC Tyr 525	GTC Val	AGC Ser	CAG Gln	ACC Thr	TCG Ser 530	CAG Gln	GAG Glu	GGC Gly	GCG Ala	GCG Ala 535	1697
45	GCG Ala	GCT Ala	GCG Ala	GAG Glu	CCC Pro 540	ATG Met	GGC Gly	CGC Arg	CCG Pro	GTG Val 545	CAG Gln	GAG Glu	GAG Glu	ACC Thr	CTG Leu 550	GCG Ala	1745
50	CGC Arg	CGA Arg	Asp	TCC Ser 555	TTC Phe	GCG Ala	GGG Gly	AAC Asn	GGC Gly 560	CCG Pro	CGC Arg	TTC Phe	CCG Pro	GAC Asp 565	CCG Pro	TGC Cys	1793
55	GGC Gly	Gly	CCC Pro 570	GAG Glu	GGG Gly	CTG Leu	Arg	GAG Glu 575	CCG Pro	GAG Glu	AAG Lys	GCC Ala	TCG Ser 580	AGG Arg	CCG Pro	GTG Val	1841
60	CAG Gln	GAG Glu 585	CAA (	GGC (	GGG ·	Ala	AAG Lys 590	GCT Ala	TGA	GCGC	cccc	СА Т	GGCT	GGGA	G		1888
	CCCG	AAGC	TC G	GAGC	CAGG	G CT	CGCG.	AGGG	CAG	CÁCC	GCA (	GCCT	CTGC	cc c	AGCC	CCGGC	1948

	Docket No.	2852-A
	CACCCAGGGA TCGATCGGTA CAGTCGAGGA AGACCACCCG GCATTCTCTG CCCACTTTGC	2008
5	CTTCCAGGAA ATGGGCTTTT CAGGAAGTGA ATTGATGAGG ACTGTCCCCA TGCCCACGGA	2068
3	TGCTCAGCAG CCCGCCGCAC TGGGGCAGAT GTCTCCCCTG CCACTCCTCA AACTCGCAGC	2128
	AGTAATTTGT GGCACTATGA CAGCTATTTT TATGACTATC CTGTTCTGTG GGGGGGGGT	2188
10	CTATGTTTC CCCCCATATT TGTATTCCTT TTCATAACTT TTCTTGATAT CTTTCCTCCC	2248
	TCTTTTTAA TGTAAAGGTT TTCTCAAAAA TTCTCCTAAA GGTGAGGGTC TCTTTCTTTT	2308
15	CTCTTTTCCT TTTTTTTTC TTTTTTTGGC AACCTGGCTC TGGCCCAGGC TAGAGTGCAG	2368
	TGGTGCGATT ATAGCCCGGT GCAGCCTCTA ACTCCTGGGC TCAAGCAATC CAAGTGATCC	2428
	TCCCACCTCA ACCTTCGGAG TAGCTGGGAT CACAGCTGCA GGCCACGCCC AGCTTCCTCC	2488
20	CCCCGACTCC CCCCCCCAG AGACACGGTC CCACCATGTT ACCCAGCCTG GTCTCAAACT	2548
	CCCCAGCTAA AGCAGTCCTC CAGCCTCGGC CTCCCAAAGT ACTGGGATTA CAGGCGTGAG	2608
25	CCCCACGCT GGCCTGCTTT ACGTATTTTC TTTTGTGCCC CTGCTCACAG TGTTTTAGAG	2668
	ATGGCTTTCC CAGTGTGTGT TCATTGTAAA CACTTTTGGG AAAGGGCTAA ACATGTGAGG	2728
	CCTGGAGATA GTTGCTAAGT TGCTAGGAAC ATGTGGTGGG ACTTTCATAT TCTGAAAAAT	2788
30	GTTCTATATT CTCATTTTTC TAAAAGAAAG AAAAAAGGAA ACCCGATTTA TTTCTCCTGA	2848
	ATCTTTTAA GTTTGTGTCG TTCCTTAAGC AGAACTAAGC TCAGTATGTG ACCTTACCCG	2908
35	CTAGGTGGTT AATTTATCCA TGCTGGCAGA GGCACTCAGG TACTTGGTAA GCAAATTTCT	2968
	AAAACTCCAA GTTGCTGCAG CTTGGCATTC TTCTTATTCT AGAGGTCTCT CTGGAAAAGA	3028
	TGGAGAAAT GAACAGGACA TGGGGCTCCT GGAAAGAAAG GGCCCGGGAA GTTCAAGGAA	3088
40	GAATAAAGTT GAAATTTTAA AAAAAAA	3115
	(2) INFORMATION FOR SEQ ID NO:2:	
45	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 591 amino acids</li><li>(B) TYPE: amino acid</li></ul>	
50	(D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: protein	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
55	Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu Lys His Tyr Glu 1 5 10 15	
	His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly Lys Tyr Met Ser	
60	Ser Lys Cys Thr Thr Thr Ser Asp Ser Val Cys Leu Pro Cys Gly Pro 35 40 45	

### **IMMUNEX CORPORATION**

Asp Glu Tyr	Leu Asp	Ser	Trp	Asn	Glu	Glu	Asp	Lys	Cys	Leu	Leu	His
50			55					60	-			

- 5 Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val Val Ala Gly Asn 65 70 75 80
- Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly Tyr His Trp Ser 85 90 95
- Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys Ala Pro Gly Leu 100 105 110
- Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr Val Cys Lys Pro 115 120 125
  - Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser Thr Asp Lys Cys 130 135 140
- 20 Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg Val Glu His His 145 150 155 160
- Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser Leu Pro Ala Arg
  165 170 175
- Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly Leu Ile Ile Leu 180 185 190
- Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile Ile Phe Gly Val 195 200 205
  - Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn Leu Trp His Trp 210 215 220
- 35 Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys Glu Ser Ser Gly 225 230 235 240
- Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly Gln Gln Gly Ala 245 250 255
  - Cys Glu Gly Val Leu Leu Leu Thr Leu Glu Glu Lys Thr Phe Pro Glu 260 265 270
- Asp Met Cys Tyr Pro Asp Gln Gly Gly Val Cys Gln Gly Thr Cys Val
  275 280 285
  - Gly Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg Met Leu Ser Leu 290 295 300
- Val Ser Lys Thr Glu Ile Glu Glu Asp Ser Phe Arg Gln Met Pro Thr 305 310 315 320
  - Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr Asp Gln Leu Leu 325 330 335
  - Phe Leu Thr Glu Pro Gly Ser Lys Ser Thr Pro Pro Phe Ser Glu Pro 340 345 350
- 60 Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln Cys Phe Thr Gly Thr

	IMi	MUNE	X CO	RPOF	RATIO	N										Docket No	ຸ່ງດ	52 4
	Glı	n Ser 370	Thr	Val	. Gly	' Ser	Glu 375	ı Se:	r Cys	a Asr	Cys	380	Glu	ı Pro	Leu	Cys	J. 20	32 <b>-</b> A
5	Arg 385	Thr	Asp	Trp	Thr	9rc 390	Met	: Sei	r Ser	Glu	Asn 395	Tyr	Let	Gln	Lys	Glu 400		
	Va]	l Asp	Ser	Gly	His 405	Cys	Pro	His	s Trp	Ala 410		Ser	Pro	Ser	Pro 415	Asn		
10	Trp	Ala	Asp	Val 420	Cys	Thr	Gly	Суз	Arg 425	Asn	Pro	Pro	Gly	Glu 430		Cys		
15	Glu	Pro	Leu 435	Val	Gly	Ser	Pro	Lys 440	Arg	Gly	Pro	Leu	Pro 445		Cys	Ala		
	Tyr	Gly 450	Met	Gly	Leu	Pro	Pro 455	Glu	Glu	Glu	Ala	Ser 460	Arg	Thr	Glu	Ala		
20	Arg 465	Asp	Gln	Pro	Glu	Asp 470	Gly	Ala	Asp	Gly	Arg 475	Leu	Pro	Ser	Ser	Ala 480		
	Arg	Ala	Gly	Ala	Gly 485	Ser	Gly	Ser	Ser	Pro 490	Gly	Gly	Gln	Ser	Pro 495	Ala		
25	Ser	Gly	Asn	Val 500	Thr	Gly	Asn	Ser	Asn 505	Ser	Thr	Phe	Ile	Ser 510	Ser	Gly		
30	Gln	Val	Met 515	Asn	Phe	Lys	Gly	Asp 520	Ile	Ile	Val	Val	Туг 525	Val	Ser	Gln		
	Thr	Ser 530	Gln	Glu	Gly	Ala	Ala 535	Ala	Ala	Ala	Glu	Pro 540	Met	Gly	Arg	Pro		
35	Val 545	Gln	Glu	Glu	Thr	Leu 550	Ala	Arg	Arg		Ser 555	Phe	Ala	Gly		Gly 560		
	Pro	Arg	Phe	Pro	Asp 565	Pro	Cys	Gly	Gly	Pro 570	Glu	Gly	Leu		Glu 575	Pro		
40	Glu	Lys	Ala	Ser 580	Arg	Pro	Val	Gln	Glu 585	Gln	Gly	Gly .		Lys . 590	Ala			
45	(2)	INFO	SEQ	UENC:	Е СН	ARAC'	TERI	STIC	S:									
50			(B (C	) TY: ) ST:	NGTH PE: 1 RANDI POLOO	nucle EDNE:	eic a SS: s	acid sing	pair: le	5								
		(ii)	MOL	ECULI	Е ТҮ!	?E: d	DNA											
55	(	iii)	HYPO	OTHE?	ricai	ւ: No	)											
55		(iv)	ANT	(-SE1	NSE:	NO												
60		(vi)			SOU SANIS			SAP	IENS									
30	( •	vii)	IMME	DIAT	re so	URCE	2 :											

185

### IMMUNEX CORPORATION

Docket No. 2852-A

- (A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS
- (B) CLONE: 9D-15C

### (ix) FEATURE:

5

- (A) NAME/KEY: CDS
- (B) LOCATION: 39..1391

	(xi)	SEQUENCE	DESCRIPTION:	CEO.	TD	NO. 2.
1.0	(311)	PPOOPINGE	DESCRIBITON:	SEU	TD	NO:3:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:																	
	CC	GCTG.	AGGC	CGC	GGCG	CCC (	GCCA	GCCT	GT C	CCGC	GCC .	ATG Met 1	GCC (	CCG Pro	CGC Arg	GCC Ala 5	53
15	CG( Arg	G CGG	G CG0 g Aro	C CGC g Arg	C CCC g Pro	) Let	G TTO 1 Phe	GCC Ala	G CTO	G CTO Let 15	ı Le	G CTO	C TGO	C GCG	G CTG a Le	G CTC u Leu 0	101
20	GCC Ala	C CGC	G CTO	G CAC u Glr 25	ı Val	G GCT L Ala	TTC Leu	G CAG	ATC 11e	≥ Ala	r cci	CCA Pro	A TGT o Cys	T ACC	: Se:	r GAG c Glu	149
25	AAC Lys	CAT His	ТАТ Туг 40	GIU	CAT His	CTC Leu	GGA Gly	CGG Arg 45	Суз	TG1 Cys	AAC Asr	AAA Lys	TGT Cys 50	Gli	A CCA	A GGA D Gly	197
30	AAG Lys	TAC Tyr 55	met	TCT Ser	TCT Ser	'AAA 'Lys	TGC Cys 60	Thr	ACT Thr	ACC Thr	TCT Ser	GAC Asp 65	Ser	GTA Val	TGT Cys	CTG Leu	245
	CCC Pro 70	Cys	GGC Gly	CCG Pro	GAT Asp	GAA Glu 75	Tyr	TTG Leu	GAT Asp	AGC Ser	TGG Trp 80	AAT Asn	GAA Glu	GAA Glu	GAT Asp	AAA Lys 85	293
35	TGC Cys	TTG Leu	CTG Leu	CAT His	AAA Lys 90	GTT Val	TGT Cys	GAT Asp	ACA Thr	GGC Gly 95	AAG Lys	GCC Ala	CTG Leu	GTG Val	GCC Ala 100	GTG Val	341
40	GTC Val	GCC Ala	GGC Gly	AAC Asn 105	AGC Ser	ACG Thr	ACC Thr	CCC Pro	CGG Arg 110	CGC Arg	TGC Cys	GCG Ala	TGC Cys	ACG Thr 115	GCT Ala	GGG Gly	389
45	TAC Tyr	CAC His	TGG Trp 120	AGC Ser	CAG Gln	GAC Asp	TGC Cys	GAG Glu 125	TGC Cys	TGC Cys	CGC Arg	CGC Arg	AAC Asn 130	ACC Thr	GAG Glu	TGC Cys	437
50	GCG Ala	CCG Pro 135	GGC Gly	CTG Leu	GGC Gly	GCC Ala	CAG Gln 140	CAC His	CCG Pro	TTG Leu	CAG Gln	CTC Leu 145	AAC Asn	AAG Lys	GAC Asp	ACA Thr	485
	GTG Val 150	TGC Cys	AAA Lys	CCT Pro	TGC Cys	CTT Leu 155	GCA Ala	GGC Gly	TAC Tyr	TTC Phe	TCT Ser 160	GAT Asp	GCC Ala	TTT Phe	TCC Ser	TCC Ser 165	533
55	ACG Thr	GAC Asp	AAA Lys	TGC Cys	AGA Arg 170	CCC Pro	TGG Trp	ACC Thr	AAC Asn	TGT Cys 175	ACC Thr	TTC Phe	CTT Leu	GGA Gly	AAG Lys 180	AGA Arg	581
60	GTA Val	GAA Glu	CAT His	CAT His	GGG Gly	ACA Thr	GAG Glu	AAA Lys	TCC Ser	GAT Asp	GCG Ala	GTT Val	TGC Cvs	AGT Ser	TCT	TCT	629

195

Val Glu His His Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser

### Docket No. 2852-A CTG CCA GCT AGA AAA CCA CCA AAT GAA CCC CAT GTT TAC TTG CCC GGT 677 Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly 200 205 725 Leu Ile Ile Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile 220 10 ATC TTT GGC GTT TGC TAT AGG AAA AAA GGG AAA GCA CTC ACA GCT AAT 773 Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn 235 240 TTG TGG CAC TGG ATC AAT GAG GCT TGT GGC CGC CTA AGT GGA GAT AAG 821 15 Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys 255 GAG TCC TCA GGT GAC AGT TGT GTC AGT ACA CAC ACG GCA AAC TTT GGT 869 Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly 20 265 CAG CAG GGA GCA TGT GAA GGT GTC TTA CTG CTG ACT CTG GAG GAG AAG 917 Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu Thr Leu Glu Glu Lys 280 285 ACA TTT CCA GAA GAT ATG TGC TAC CCA GAT CAA GGT GGT GTC TGT CAG 965 Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln Gly Gly Val Cys Gln 295 300 GGC ACG TGT GTA GGA GGT GGT CCC TAC GCA CAA GGC GAA GAT GCC AGG 1013 Gly Thr Cys Val Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg 310 315 320 ATG CTC TCA TTG GTC AGC AAG ACC GAG ATA GAG GAA GAC AGC TTC AGA 1061 35 Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu Glu Asp Ser Phe Arg 340 CAG ATG CCC ACA GAA GAT GAA TAC ATG GAC AGG CCC TCC CAG CCC ACA 1109 Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr 40 345 GAC CAG TTA CTG TTC CTC ACT GAG CCT GGA AGC AAA TCC ACA CCT CCT 1157 Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser Lys Ser Thr Pro Pro 365 45 TTC TCT GAA CCC CTG GAG GTG GGG GAG AAT GAC AGT TTA AGC CAG TGC 1205 Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln Cys 50 TTC ACG GGG ACA CAG AGC ACA GTG GGT TCA GAA AGC TGC AAC TGC ACT 1253 Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu Ser Cys Asn Cys Thr GAG CCC CTG TGC AGG ACT GAT TGG ACT CCC ATG TCC TCT GAA AAC TAC 1301 55 Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met Ser Ser Glu Asn Tyr 410 TTG CAA AAA GAG GTG GAC AGT GGC CAT TGC CCG CAC TGG GCA GCC AGC 1349 Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro His Trp Ala Ala Ser 60 425 430



### **IMMUNEX CORPORATION**

Docket No. 2852-A

CCC AGC CCC AAC TGG GCA GAT GTC TGC ACA GGC TGC CGG AAC
Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly Cys Arg Asn
440
445

1391

5

10

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 451 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
  - Met Ala Pro Arg Ala Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu 1 5 10 15
- 20 Leu Cys Ala Leu Leu Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro 20 25 30
  - Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn
    35 40 45
  - Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser 50 60
- Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp 65 70 75 80
  - Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys 85 90 95
- 35 Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys 100 105 110
- Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg 115 120 125
  - Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln
    130 135 140
- Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser 145 150 155 160
  - Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr 165 170 175
- 50 Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala 180 185 190
  - Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His 195 200 205
    - Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala 210 215 220
- Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys 225 230 235 240

	Ala	ı Lei	ı Thr	: Ala	245	Leu	Trp	His	Trp	250	Asn	Gli	ı Ala	Cys	G1 <sub>y</sub> 255	/ Arg
5	Leu	ı Ser	Gly	260	Lys	Glu	Ser	Ser	Gly 265	Asp	Ser	Cys	: Val	Ser 270		His
	Thr	Ala	Asn 275	Phe	Gly	Gln	Gln	Gly 280	Ala	Cys	Glu	Gly	Val 285		Leu	Leu
10	Thr	Leu 290	Glu	Glu	Lys	Thr	Phe 295	Pro	Glu	Asp	Met	Cys 300		Pro	Asp	Gln
15	Gly 305	Gly	Val	Cys	Gln	Gly 310	Thr	Cys	Val	Gly	Gly 315	Gly	Pro	Tyr	Ala	Gln 320
13	Gly	Glu	Asp	Ala	Arg 325	Met	Leu	Ser	Leu	Val 330	Ser	Lys	Thr	Glu	Ile 335	Glu
20	Glu	Asp	Ser	Phe 340	Arg	Gln	Met	Pro	Thr 345	Glu	Asp	Glu	Tyr	Met 350	Asp	Arg
	Pro	Ser	Gln 355	Pro	Thr	Asp	Gln	Leu 360	Leu	Phe	Leu	Thr	Glu 365	Pŗo	Gly	Ser
25	Lys	Ser 370	Thr	Pro	Pro	Phe	Ser 375	Glu	Pro	Leu	Glu	Val 380	Gly	Glu	Asn	Asp
30	Ser 385	Leu	Ser	Gln	Cys	Phe 390	Thr	Gly ·	Thr	Gln	Ser 395	Thr	Val	Gly	Ser	Glu 400
50	Ser	Cys	Asn	Cys	Thr 405	Glu	Pro	Leu	Суѕ	Arg 410	Thr	Asp	Trp	Thr	Pro 415	Met
35	Ser	Ser	Glu	Asn 420	Tyr	Leu	Gln	Lys	Glu 425	Val	Asp	Ser	Gly	His 430	Cys	Pro
	His	Trp	Ala 435	Ala	Ser	Pro	Ser	Pro 440	Asn	Trp	Ala	Asp	Val 445	Cys	Thr	Gly
40	Cys	Arg 450	Asn													
45	(2)	INFC	RMAT	NOI	FOR	SEQ	ID N	0:5:								
		(i)	(A	.) LE	NGTH	: 31	TERI	ase ;	pair	s						
50			(C	) ST	RAND	EDNE.	eic a SS: a linea	sing	le							
		(ii)	MOL	ECUL	E TY	PE:	cDNA									
55	(	iii)	НҮР	отне	TICA	L: NO	<b>o</b>									
JJ		(iv)	ANT	I-SE	NSE:	NO										
60		(vi)		GINA:			: HOMO	SAP	IENS							
00	(-	vii)	IMM	EDIA	re so	OURCE	3:									

Docket No. 2852-A





Docket No. 2852-A

- (A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS
- (B) CLONE: FULL LENGTH RANK

### (ix) FEATURE:

5

- (A) NAME/KEY: CDS
  (B) LOCATION: 39..1886

 (xi)	SEQUENCE	DESCRIPTION:	SEO	ID	NO:5:

10		(x	i) S	EQUE	NCE I	DESC	RIPT	ON:	SEQ	ID I	NO:5	:						
	CCC	GCTG.	AGGC	CGC	GGCG(	CCC (	GCCAC	SCCTO	GT CO	CCGC				CCG ( Pro <i>l</i>				53
15	CGC Arg	G CGG J Arg	G CG(	C CGC g Arg	C CCC g Pro 10	Leu	F TTC ı Ph∈	GCC Ala	G CTC	G CTO Leo 15	ı Let	G CT(	TG0	C GCC s Ala	G CTO a Leu 20	G CTC Leu )		101
20	GCC Ala	C CGO	G CTO	G CAC 1 Glr 25	ı Val	GCT Ala	TTC Leu	CAG Glr	30	: Ala	r cci	CCA Pro	A TG	T ACC Thr 35	Ser	GAG Glu		149
25	AAG Lys	CAT His	TAT TY1	Glu	CAT His	CTC	GGA Gly	CGG Arg 45	Cys	TGT Cys	T AAC s Asn	AAA Lys	TG1 Cys	Glu	CCA Pro	GGA Gly		197
30	AAG Lys	ТАС Тук 55	Met	TCT Ser	TCT Ser	AAA Lys	TGC Cys 60	Thr	ACT Thr	ACC Thr	TCT Ser	GAC Asp 65	Ser	GTA Val	TGT Cys	CTG Leu		245
	CCC Pro 70	Cys	Gly Gly	CCG Pro	GAT Asp	GAA Glu 75	TAC Tyr	TTG Leu	GAT Asp	AGC Ser	TGG Trp 80	AAT Asn	GAA Glu	GAA Glu	GAT Asp	AAA Lys 85		293
35	TGC Cys	TTG Leu	CTG Leu	CAT His	AAA Lys 90	GTT Val	TGT Cys	GAT Asp	ACA Thr	GGC Gly 95	AAG Lys	GCC Ala	CTG Leu	GTG Val	GCC Ala 100	GTG Val	:	341
40	GTC Val	GCC Ala	GGC Gly	AAC Asn 105	AGC Ser	ACG Thr	ACC Thr	CCC Pro	CGG Arg 110	CGC Arg	TGC Cys	GCG Ala	TGC Cys	ACG Thr 115	GCT Ala	GGG Gly	;	389
45	TAC Tyr	CAC His	TGG Trp 120	AGC Ser	CAG Gln	GAC Asp	TGC Cys	GAG Glu 125	TGC Cys	TGC Cys	CGC Arg	CGC Arg	AAC Asn 130	ACC Thr	GAG Glu	TGC Cys		437
50	GCG Ala	CCG Pro 135	GGC Gly	CTG Leu	GGC Gly	GCC Ala	CAG Gln 140	CAC His	CCG Pro	TTG Leu	CAG Gln	CTC Leu 145	AAC Asn	AAG Lys	GAC Asp	ACA Thr	4	185
	GTG Val 150	TGC Cys	AAA Lys	CCT Pro	TGC Cys	CTT Leu 155	GCA Ala	GGC Gly	TAC Tyr	TTC Phe	TCT Ser 160	GAT Asp	GCC Ala	TTT Phe	TCC Ser	TCC Ser 165	5	33
55	ACG Thr	GAC Asp	AAA Lys	TGC Cys	AGA Arg 170	CCC Pro	TGG Trp	ACC Thr	AAC Asn	TGT Cys 175	ACC Thr	TTC Phe	CTT Leu	GGA Gly	AAG Lys 180	AGA Arg	5	81
60	GTA Val	GAA Glu	CAT His	CAT His 185	GGG Gly	ACA Thr	GAG Glu	Lys	TCC Ser 190	GAT Asp	GCG Ala	GTT Val	TGC Cys	AGT Ser	TCT Ser	TCT Ser	6	29

_	CT( Le	G CC u Pr	A GC o Al 20	a Ar	A AAA	A CCA	A CCA	AAC Asi 205	n Gli	A CC	C CA'	T GT s Va	г та 1 ту 21	r Le	G CC u Pr	C GGT o Gly	677
5	TT? Lei	A AT. 11 21	e II	T CTO	G CT:	r CTC	TTC Phe 220	Ala	G TCT a Ser	GT(	G GCC l Ala	C CTC a Let 225	G GTO	G GC	r GCC	C ATC	725
10	AT0 I1€ 230	Pn	T GGG e Gl	C GTT y Val	TGC Cys	TAT Tyr 235	Arg	AAA Lys	A AAA 5 Lys	GG(	3 AA# 7 Lys 240	s Ala	A CTO	C AC	A GC:	r AAT a Asn 245	773
15	TTC Leu	TG(	G CAG P His	C TGG Trp	ATC 11e 250	Asn	GAG Glu	GCT Ala	TGT Cys	GG( G1) 255	/ Arg	CTA Leu	AGT Sei	r GG/	A GAT Asg 260	T AAG D Lys	821
20	GAG Glu	TC(	C TCA Ser	GGT Gly 265	Asp	AGT Ser	TGT Cys	GTC Val	Ser 270	ACA Thr	CAC His	ACG Thr	GCA Ala	A AAC Asr 275	Phe	GGT Gly	869
25	CAG Gln	Glr	G GGA 1 Gly 280	' Ala	TGT Cys	GAA Glu	GGT Gly	GTC Val 285	TTA Leu	CTG Leu	CTG Leu	ACT Thr	CTG Leu 290	Glu	GAG Glu	AAG Lys	917
	ACA Thr	TT1 Phe 295	Pro	GAA Glu	GAT Asp	ATG Met	TGC Cys 300	TAC Tyr	CCA Pro	GAT Asp	CAA Gln	GGT Gly 305	GGT Gly	GTC Val	TGT Cys	CAG Gln	965
30	GGC Gly 310	Thr	TGT Cys	GTA Val	GGA Gly	GGT Gly 315	GGT Gly	CCC Pro	TAC Tyr	GCA Ala	CAA Gln 320	GGC Gly	GAA Glu	GAT Asp	GCC Ala	AGG Arg 325	1013
35	ATG Met	CTC Leu	TCA Ser	TTG Leu	GTC Val 330	AGC Ser	AAG Lys	ACC Thr	GAG Glu	ATA Ile 335	GAG Glu	GAA Glu	GAC Asp	AGC Ser	TTC Phe 340	AGA Arg	1061
40	CAG Gln	ATG Met	CCC Pro	ACA Thr 345	GAA Glu	GAT Asp	GAA Glu	TAC Tyr	ATG Met 350	GAC Asp	AGG Arg	CCC Pro	TCC Ser	CAG Gln 355	CCC Pro	ACA Thr	1109
45	GAC Asp	CAG Gln	TTA Leu 360	CTG Leu	TTC Phe	CTC Leu	ACT Thr	GAG Glu 365	CCT Pro	GGA Gly	AGC Ser	AAA Lys	TCC Ser 370	ACA Thr	CCT Pro	CCT Pro	1157
	TTC Phe	TCT Ser 375	GAA Glu	CCC Pro	CTG Leu	GAG Glu	GTG Val 380	GGG Gly	GAG Glu	AAT Asn	GAC Asp	AGT Ser 385	TTA Leu	AGC Ser	CAG Gln	TGC Cys	1205
50	TTC Phe 390	ACG Thr	GGG Gly	ACA Thr	CAG Gln	AGC Ser 395	ACA (	GTG Val	GGT Gly	TCA Ser	GAA Glu 400	AGC Ser	TGC Cys	AAC Asn	TGC Cys	ACT Thr 405	1253
55	GIU	Pro	Leu	Суѕ	Arg 410	Thr	GAT ' Asp '	ľrp	Thr	Pro 415	Met	Ser	Ser	Glu	Asn 420	Tyr	1301
60	TTG Leu	CAA Gln	AAA Lys	GAG Glu 425	GTG Val	GAC . Asp	AGT ( Ser (	3ly	CAT ' His ( 430	IGC Cys	CCG   Pro	CAC ' His '	TGG Trp	GCA Ala 435	GCC Ala	AGC Ser	1349

	IMN	1UNE	х со	RPOR	RATIC	N										Docket	No. 2852-A
	CCC Pro	AGC Ser	CCC Pro 440	Asn	TGG Trp	GCA Ala	GAT Asp	GTC Val 445	. Cys	ACA Thr	GG(	TGC Cys	CGC Arg 450	Asn	CCT	CCT Pro	1397
5	GGG Gly	GAG Glu 455	Asp	TGT Cys	GAA Glu	CCC Pro	CTC Leu 460	GTG Val	GGT Gly	TCC Ser	CCA Pro	A AAA Lys 465	Arg	GGA Gly	CCC Pro	TTG Leu	1445
10	CCC Pro 470	CAG Gln	TGC Cys	GCC Ala	тат туг	GGC Gly 475	ATG Met	GGC Gly	CTT Leu	CCC Pro	CCT Pro 480	GAA Glu	GAA Glu	GAA Glu	GCC Ala	AGC Ser 485	1493
15	AGG Arg	ACG Thr	GAG Glu	GCC Ala	AGA Arg 490	GAC Asp	CAG Gln	CCC Pro	GAG Glu	GAT Asp 495	Gly	GCT Ala	GAT Asp	GGG Gly	AGG Arg 500	CTC Leu	1541
20	CCA Pro	AGC Ser	TCA Ser	GCG Ala 505	AGG Arg	GCA Ala	GGT Gly	GCC Ala	GGG Gly 510	TCT Ser	GGA Gly	AGC Ser	TCC Ser	CCT Pro 515	GGT Gly	GGC Gly	1589
	CAG Gln	TCC Ser	CCT Pro 520	GCA Ala	TCT Ser	GGA Gly	AAT Asn	GTG Val 525	ACT Thr	GGA Gly	AAC Asn	AGT Ser	AAC Asn 530	TCC Ser	ACG Thr	TTC Phe	1637
25	ATC Ile	TCC Ser 535	AGC Ser	GGG Gly	CAG Gln	GTG Val	ATG Met 540	AAC Asn	TTC Phe	AAG Lys	GGC Gly	GAC Asp 545	ATC Ile	ATC Ile	GTG Val	GTC Val	1685
30	TAC Tyr 550	GTC Val	AGC Ser	CAG Gln	ACC Thr	TCG Ser 555	CAG Gln	GAG Glu	GGC Gly	GCG Ala	GCG Ala 560	GCG Ala	GCT Ala	GCG Ala	GAG Glu	CCC Pro 565	1733
35	ATG Met	GGC Gly	CGC Arg	CCG Pro	GTG Val 570	CAG Gln	GAG Glu	GAG Glu	ACC Thr	CTG Leu 575	GCG Ala	CGC Arg	CGA Arg	GAC Asp	TCC Ser 580	TTC Phe	1781
40	GCG Ala	GGG Gly	AAC Asn	GGC Gly 585	CCG Pro	CGC Arg	TTC Phe	CCG Pro	GAC Asp 590	CCG Pro	TGC Cys	GGC Gly	GGC Gly	CCC Pro 595	GAG Glu	GGG Gly	1829
	CTG Leu	CGG Arg	GAG Glu 600	CCG Pro	GAG Glu	AAG Lys	Ala	TCG Ser 605	AGG Arg	CCG Pro	GTG Val	CAG Gln	GAG Glu 610	CAA ( Gln (	GGC Gly	GGG Gly	1877
45	GCC Ala	AAG Lys 615	GCT Ala	TGAG	CGCC	cc c	CATG	GCTG	G GA	GCCC	GAAG	CTC	GGAG	CCA			1926
50	GGGC	TCGC	GA G	GGCA	GCAC	C GC	AGCC'	ГСТG	CCC	CAGC	CCC	GGCC	ACCC	AG GO	GATC	GATCG	1986
50	GTAC.	AGTC	GA G	GAAG	ACCA	c cc	GGCA'	rtct	CTG	CCCA	СТТ	TGCC	rtcc.	AG G	YTAA.	GGCT	2046
	TTTC	AGGA	AG T	GAAT"	TGAT	G AG	GACT	GTCC	CCA	rgcc	CAC	GGAT	GCTC	AG C	AGCC	CGCCG	2106
55	CACTY	GGGG	CA G	ATGT	CTCC	C CT	GCCA	CTCC	TCA	AACT	CGC .	AGCAG	GTAA'	TT TO	TGG	CACTA	2166
	TGAC	AGCT.	AT T	TTTA:	TGAC'	T ATO	CCTGT	TCT	GTG	GGGG	GGG (	GGTC1	ratgʻ	rr ra	rccc	CCAT	2226
60	YTTTA	GTAT'	TC C	TTTT(	CATA	A CT	rttci	rtga	ТАТС	CTTT	CCT (	CCCTC	CTTT	TT TA	ATG	DAAAG	2286
	GTTT	CTC	AA AA	<b>A</b> ATT(	CTCC'	T AA	AGGTC	SAGG	GTCT	CTT	rct '	rttci	CTT:	rr cc	TTT	ГТТТТ	2346

	IMMUNEX CORPORATION Docket No.	2852-A
	TTCTTTTTT GGCAACCTGG CTCTGGCCCA GGCTAGAGTG CAGTGGTGCG ATTATAGCCC	2406
5	GGTGCAGCCT CTAACTCCTG GGCTCAAGCA ATCCAAGTGA TCCTCCCACC TCAACCTTCG	2466
	GAGTAGCTGG GATCACAGCT GCAGGCCACG CCCAGCTTCC TCCCCCGAC TCCCCCCCC	2526
	CAGAGACACG GTCCCACCAT GTTACCCAGC CTGGTCTCAA ACTCCCCAGC TAAAGCAGTC	2586
10	CTCCAGCCTC GGCCTCCCAA AGTACTGGGA TTACAGGCGT GAGCCCCCAC GCTGGCCTGC	2646
	TTTACGTATT TTCTTTTGTG CCCCTGCTCA CAGTGTTTTA GAGATGGCTT TCCCAGTGTG	2706
15	TGTTCATTGT AAACACTTTT GGGAAAGGGC TAAACATGTG AGGCCTGGAG ATAGTTGCTA	2766
	AGTTGCTAGG AACATGTGGT GGGACTTTCA TATTCTGAAA AATGTTCTAT ATTCTCATTT	2826
	TTCTAAAAGA AAGAAAAAAG GAAACCCGAT TTATTTCTCC TGAATCTTTT TAAGTTTGTG	2886
20	TCGTTCCTTA AGCAGAACTA AGCTCAGTAT GTGACCTTAC CCGCTAGGTG GTTAATTTAT	2946
	CCATGCTGGC AGAGGCACTC AGGTACTTGG TAAGCAAATT TCTAAAACTC CAAGTTGCTG	3006
25	CAGCTTGGCA TTCTTCTTAT TCTAGAGGTC TCTCTGGAAA AGATGGAGAA AATGAACAGG	3066
	ACATGGGGCT CCTGGAAAGA AAGGGCCCGG GAAGTTCAAG GAAGAATAAA GTTGAAATTT	3126
	ТААААААА	3136
30	(2) INFORMATION FOR SEQ ID NO:6:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 616 amino acids (B) TYPE: amino acid	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
	Met Ala Pro Arg Ala Arg Arg Arg Pro Leu Phe Ala Leu Leu 1 5 10 15	
45	Leu Cys Ala Leu Leu Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro 20 25 30	
50	Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn 35 40 45	
- •	Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser 50 55 60	
55	Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp	

Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys
85 90 95

Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys

	••••		LAC		IXA I IV	ON										Docket
	Al	а Су	s Th	r Al 5	a Gly	у Туз	c Hi	s Tr 12	p Se 0	r Gl	n As	р Су:	s Gl 12		s Cy:	s Arg
5	Ar	g As 13	n Th 0	r Gl	u Cys	s Ala	13	o G1; 5	y Le	u Gl	y Ala	a Glr 140	n Hi	s Pr	o Lei	u Gln
10	Le: 14!	u As 5	n Ly	s As	p Thi	r Val	L Cy:	s Ly	s Pro	э Су	s Lei 159		a Gl	у Ту	r Phe	e Ser 160
	Asp	o Al	a Pho	e Sei	r Ser 165	Thr	As <sub>I</sub>	o Ly:	s Cys	3 Ar		Trp	Th	r Asr	1 Cys	Thr
15	Ph€	e Le	u Gly	y Lys 180	s Arg	y Val	Glu	ı His	s His 185	Gl <sub>y</sub>	y Thr	Glu	ı .Lys	Ser 190		Ala
			195	•	•			200	)				205	5		His
20		210	J				215	•				220				Ala
25	223	l			Ile	230					235					240
	Ala	Leu	ı Thr	Ala	Asn 245	Leu	Trp	His	Trp	I1∈ 250		Glu	Ala	Cys	Gly 255	Arg
30				260					265					270		
25			2/5		Gly			280					285			
35		290			Lys		295					300		•		
40	202				Gln	310					315					320
					Arg 325					330					335	
45				240	Arg				345					350		
50			333		Thr			360					365			
50		370			Pro		375					380				
55	505					390					395					400
					Thr 405					410					415	
60	Ser	Ser	Glu	Asn 420	Tyr	Leu (	Gln	Lys	Glu 425	Val	Asp :	Ser (		His (	Cys	Pro

	IMI	MUNE	X CC	RPOF	RATIO	N										Doolest No. 2000 4
	His	s Trp	Ala 435	a Ala	Ser	Pro	Ser	Pro 440	Asn	Trp	Ala	Asp	Val 445	Cys	Thr	Docket No. 2852-A
5	Cys	450	Asn	Pro	Pro	Gly	Glu 455	Asp	Cys	Glu	Pro	Leu 460	Val	Gly	Ser	Pro
	Lys 465	Arg	Gly	Pro	Leu	Pro 470	Gln	Cys	Ala	Tyr	Gly 475	Met	Gly	Leu	Pro	Pro 480
10	Glu	Glu	Glu	Ala	Ser 485	Arg	Thr	Glu	Ala	Arg 490	Asp	Gln	Pro	Glu	Asp 495	Gly
15	Ala	Asp	Gly	Arg 500	Leu	Pro	Ser	Ser	Ala 505	Arg	Ala	Gly	Ala	Gly 510	Ser	Gly
	Ser	Ser	Pro 515	Gly	Gly	Gln	Ser	Pro 520	Ala	Ser	Gly	Asn	Val 525	Thr	Gly	Asn
20	Ser	Asn 530	Ser	Thr	Phe	Ile	Ser 535	Ser	Gly	Gln	Val	Met 540	Asn	Phe	Lys	Gly
	747					550					555					560
25		Ala			265					570					575	
30		Arg		580					585					590		
		Gly	333					600	Pro	Glu	Lys		Ser 605	Arg	Pro	Val
35	Gln	Glu 610	Gln	Gly	Gly		Lys 615	Ala								
40	(2)	INFO														
40		(i)	(A (B	) LEI ) TY:	NGTH PE:	: 8 a	TERI: amino o ac:	o ac:	ids			•				
45		(ii)	(C (D	) STI ) TOI	RANDI POLO	EDNE:	SS: r linea	not :	rele	/ant						
50		vii)	IMM	EDIAT	re so	OURCE			de							
	(:	xi) s	EQUI	ENCE	DESC	CRIPT	: NOI	SEÇ	) ID	NO:7	·:					
55	Asp 1	Tyr I	ys <i>l</i>	Asp A	Asp A 5	Asp A	sp L	ys								
	(2)	ENFOF	ITAM	ON F	OR S	EQ I	D NO	:8:								
60		(i)	(A)	LEN	GTH:	232	ERIS ami aci	no a	: cids							

- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: Human
  - (vii) IMMEDIATE SOURCE:
  - (B) CLONE: IgG1 Fc mutein
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
- Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
  15 1 5 10 15
  - Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro 20 25 30
- 20 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val 35 40 45
  - Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val 50 55 60
  - Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln 65 70 75 80
- Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln 85 90 95
  - Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala 100 105 110
- 35 Leu Pro Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro 115 120 125
- Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
  130 135 140
  - Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg 145 150 155 160
- His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
  165 170 175
  - Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr 180 185 190
- Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
  195 200 205
- Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
  210 215 220
  - Ser Leu Ser Leu Ser Pro Gly Lys 225 230
- 60 (2) INFORMATION FOR SEQ ID NO:9:

### Docket No. 2852-A (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: not relevant 5 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (iii) HYPOTHETICAL: NO 10 (iv) ANTI-SENSE: NO (vi) ORIGINAL SOURCE: (A) ORGANISM: CMV (R2780 Leader) 15 (ix) FEATURE: (D) OTHER INFORMATION: Met1-Arg28 is the actual leader peptide; Arg29 strengthens the furin cleavage site; nucleotides encoding Thr30 and Ser31 add a Spel site. 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9: Met Ala Arg Arg Leu Trp Ile Leu Ser Leu Leu Ala Val Thr Leu Thr 10 25 Val Ala Leu Ala Ala Pro Ser Gln Lys Ser Lys Arg Arg Thr Ser 30 (2) INFORMATION FOR SEQ ID NO:10: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1630 base pairs (B) TYPE: nucleic acid 35 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA 40 (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (vi) ORIGINAL SOURCE: 45 (A) ORGANISM: Mus musculus (vii) IMMEDIATE SOURCE: (A) LIBRARY: (B) CLONE: RANKL 50 (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 3..884 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: CC GGC GTC CCA CAC GAG GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro 47 60 5 10

		IM	MUN	EX C	ORPO	RATIO	NC										Docket	No. 2852-A
		GC' Ala	r cce a Pre	G GCO	G CCO a Pro	G CC D Pro 20	o Pro	C GCC D Ala	C GCG a Ala	C TCC	C CGG r Arg 2!	g Se	C ATO	G TTO	C CT	G GC u Ala 3	C CTC a Leu	95
	5	CT( Let	G GGG	G CTO	G GG/ u Gly 35	y Lei	G GGC	C CAG	G GTO n Val	GTC Val 40	l Cys	C AGO	C ATO	C GC: e Ala	CTC Lei 4!	u Ph	C CTG e Leu	143
	10	ТА( Туг	TTT Phe	CGA Arg 50	J ATS	G CAC	ATC Met	GA1 : Asp	r cci p Pro 55	) Asr	AGA Arg	A ATA	A TCZ e Sez	A GAZ r Glu 60	ı Ası	C AGO Sei	C ACT	191
	15	CAC	TGC Cys	: Ph€	TA1	AGA Arg	ATC Ile	CTC Leu 70	ı Arg	CTC Leu	CAT His	GAZ Glu	A AAC 1 Asr 75	ı Ala	GAT Asp	TTC Leu	G CAG	239
	20	GAC Asp 80	Ser	ACT Thr	CTC Leu	GAG Glu	AGT Ser 85	Glu	GAC Asp	ACA Thr	CTA Leu	CCI Pro	Asp	TCC Ser	TGC Cys	AGG Arg	AGG Arg 95	. 287
<u> </u>	20	ATG Met	AAA Lys	CAA Gln	GCC Ala	TTT Phe 100	Gln	GGG Gly	GCC Ala	GTG Val	CAG Gln 105	AAG Lys	GAA Glu	CTG Leu	CAA Gln	CAC His	ATT	335
	25	GTG Val	GGG Gly	CCA Pro	CAG Gln 115	Arg	TTC Phe	TCA Ser	GGA Gly	GCT Ala 120	CCA Pro	GCT Ala	ATG Met	ATG Met	GAA Glu 125	Gly	TCA Ser	383
	30	TGG Trp	TTG Leu	GAT Asp 130	Val	GCC Ala	CAG Gln	CGA Arg	GGC Gly 135	AAG Lys	CCT Pro	GAG Glu	GCC Ala	CAG Gln 140	CCA Pro	TTT Phe	GCA Ala	431 "
	35	CAC His	CTC Leu 145	ACC Thr	ATC Ile	AAT Asn	GCT Ala	GCC Ala 150	AGC Ser	ATC Ile	CCA Pro	TCG Ser	GGT Gly 155	TCC Ser	CAT His	AAA Lys	GTC Val	479
	40	ACT Thr 160	CTG Leu	TCC Ser	TCT Ser	TGG Trp	TAC Tyr 165	CAC His	GAT Asp	CGA Arg	GGC Gly	TGG Trp 170	GCC Ala	AAG Lys	ATC Ile	TCT Ser	AAC Asn 175	527
	.0	ATG Met	ACG Tḥr	TTA Leu	AGC Ser	AAC Asn 180	GGA Gly	AAA Lys	CTA Leu	AGG Arg	GTT Val 185	AAC Asn	CAA Gln	GAT Asp	GGC Gly	TTC Phe 190	TAT Tyr	575
	45	TAC Tyr	CTG Leu	TAC Tyr	GCC Ala 195	AAC Asn	ATT Ile	TGC Cys	TTT Phe	CGG Arg 200	CAT His	CAT His	GAA Glu	ACA Thr	TCG Ser 205	GGA Gly	AGC Ser	623
	50	GTA Val	CCT Pro	ACA Thr 210	GAC Asp	TAT Tyr	CTT Leu	CAG Gln	CTG Leu 215	ATG Met	GTG Val	TAT Tyr	GTC Val	GTT Val 220	AAA Lys	ACC Thr	AGC Ser	671
	55	TTG	AAA Lys 225	ATC Ile	CCA Pro	AGT Ser	Ser	CAT His 230	AAC Asn	CTG Leu	ATG Met	Lys	GGA Gly 235	GGG Gly	AGC Ser	ACG Thr	AAA Lys	719
	60	AAC Asn 240	TGG Trp	TCG Ser	GGC Gly	Asn	TCT Ser (	GAA Glu	TTC Phe	CAC His	Phe '	ТАТ Туг 250	TCC Ser	ATA . Ile .	AAT Asn	Val	GGG Gly 255	767

	IMMUNEX CORPORATION Docket No.	2052 A
	GGA TTT TTC AAG CTC CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser 260 265 270	2832-A 815
	AAC CCT TCC CTG CTG GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala 275 280 285	863
10	TTC AAA GTT CAG GAC ATA GAC TGAGACTCAT TTCGTGGAAC ATTAGCATGG Phe Lys Val Gln Asp Ile Asp 290	914
	ATGTCCTAGA TGTTTGGAAA CTTCTTAAAA AATGGATGAT GTCTATACAT GTGTAAGACT	974
15	ACTAAGAGAC ATGGCCCACG GTGTATGAAA CTCACAGCCC TCTCTCTTGA GCCTGTACAG	1034
	GTTGTGTATA TGTAAAGTCC ATAGGTGATG TTAGATTCAT GGTGATTACA CAACGGTTTT	1094
20	ACAATTTTGT AATGATTTCC TAGAATTGAA CCAGATTGGG AGAGGTATTC CGATGCTTAT	1154
20	GAAAAACTTA CACGTGAGCT ATGGAAGGGG GTCACAGTCT CTGGGTCTAA CCCCTGGACA	1214
	TGTGCCACTG AGAACCTTGA AATTAAGAGG ATGCCATGTC ATTGCAAAGA AATGATAGTG	1274
25	TGAAGGGTTA AGTTCTTTTG AATTGTTACA TTGCGCTGGG ACCTGCAAAT AAGTTCTTTT	1334
	TTTCTAATGA GGAGAGAAAA ATATATGTAT TTTTATATAA TGTCTAAAGT TATATTTCAG	1394
	GTGTAATGTT TTCTGTGCAA AGTTTTGTAA ATTATATTTG TGCTATAGTA TTTGATTCAA	
30	AATATTTAAA AATGTCTCAC TGTTGACATA TTTAATGTTT TAAATGTACA GATGTATTTA	1454
	ACTGGTGCAC TTTGTAATTC CCCTGAAGGT ACTCGTAGCT AAGGGGGCAG AATACTGTTT	1514
35	CTGGTGACCA CATGTAGTTT ATTTCTTTAT TCTTTTTAAC TTAATAGAGT CTTCAG	1574
	TOTAL TOTAL TAKINGAGT CTTCAG	1630
	(2) INFORMATION FOR SEQ ID NO:11:	
40	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 294 amino acids</li><li>(B) TYPE: amino acid</li><li>(D) TOPOLOGY: linear</li></ul>	
45	(ii) MOLECULE TYPE: protein	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
50	Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala 1 5 10 15	
	Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu 20 25 30	,
55	Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr 35 40 45	•
60	Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His 50 55 60	

	IM	MUN	EX C	ORPO	RATIO	NC										D1		
		s Ph					u Arg	J Le	u Hi	s Gl	ı Ası 79	n Al	a As	p Le	u Gl	Docke n Asp 80	t No. 28	52-A
5	Se:	r Th	r Le	u Glı	Sei 85	Glu 5	ı Asp	Th:	r Lei	u Pro 90	As <u>r</u>	Se:	r Cy	s Ar	g Ar	g Met		
	Lys	s Gl	n Ala	Phe 100	Glr	ı Gly	/ Ala	Va:	l Glr 105	n Lys	Glu	ı Leı	ı Glı	1 Hi		e Val		
10	.G17	/ Pro	0 Glr 115	n Arg	Phe	e Ser	Gly	Ala 120	a Pro	Ala	Met	Met	Glu 125		y Sei	Trp		
15	Leu	130	Va]	. Ala	Gln	Arg	Gly 135	Lys	Pro	Glu	Ala	Gln 140	Pro	Phe	e Ala	His		
						130					155					Thr 160		
20					105		•			170					175			
2.5				Asn 180					182					190				
25								200					205					
30		210		Tyr			215			•		220		•				
				Ser		230					235					240		
35					243					250					255			
40				Leu 260					265					270				
40			2,5	Leu .			Asp (	Gln 280	Asp .	Ala '	Thr '		Phe 285	Gly	Ala	Phe		
45	Lys	Val 290	Gln	Asp :	Ile i	Asp												
	(2)			ION 1														
50		(1)	(A (B (C	UENCE ) LEN ) TYE ) STF ) TOE	IGTH: PE: r RANDE	954 nucle DNES	1 bas eic a SS: s	e pa cid ing]	airs									
55	į	(ii)	MOL	ECULE	TYP	E: c	DNA											
				тнет														
60				-SEN SINAL														



### **IMMUNEX CORPORATION**

Docket No. 2852-A

(A) ORGANISM: Homo sapiens

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- 5 (B) CLONE: huRANKL (full length)

### (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..951

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

				_					224			۷.					
15	He	G CG t Ar	C CG	C GCG	a Sei	C AGA r Arg	A GA( J Asp	ТА( Ту	C ACC	C AAG Ly:	s Ty	C CTO	G CG	T GG g Gl	C TC y Se	G GAG r Glu 5	48
20	GA( Glu	ATO	G GGG	C GG( 7 Gl <sub>2</sub> 20	GT2	C CCC / Pro	GGA Gly	A GCC Ala	C CCC Pro 25	His	C GAC	ı Gly	C CCC	C CTC Let 30	ı Hi	C GCC s Ala	96
25	CCC Pro	CCC Pro	G CCC Pro 35	LIC	GCC Ala	CCG Pro	CAC His	CAG Gln 40	Pro	CCC Pro	GCC Ala	C GCC	TCC Sei	Arg	TC( Se)	C ATG Met	144
	TTC Phe	GT( Val	- WIC	CTC Leu	CTG Leu	GGG Gly	CTG Leu 55	GTA	CTG Leu	GGC Gly	CAG Gln	GTT Val 60	Val	TGC Cys	AGC Ser	GTC Val	192
30	GCC Ala 65	neu	TTC Phe	TTC Phe	TAT Tyr	TTC Phe 70	AGA Arg	GCG Ala	CAG Gln	ATG Met	GAT Asp 75	Pro	AAT Asn	'AGA Arg	ATA	TCA Ser 80	240
35	GAA Glu	GAT Asp	GGC Gly	ACT Thr	CAC His 85	TGC Cys	ATT Ile	TAT Tyr	AGA Arg	ATT Ile 90	TTG Leu	AGA Arg	CTC Leu	CAT	GAA Glu 95	AAT Asn	288
40	GCA Ala	GAT Asp	TTT Phe	CAA Gln 100	GAC Asp	ACA Thr	ACT Thr	CTG Leu	GAG Glu 105	AGT Ser	CAA Gln	GAT Asp	ACA Thr	AAA Lys 110	TTA Leu	ATA Ile	336
45	CCT Pro	GAT Asp	TCA Ser 115	TGT Cys	AGG Arg	AGA Arg	ATT Ile	AAA Lys 120	CAG Gln	GCC Ala	TTT Phe	CAA Gln	GGA Gly 125	GCT Ala	GTG Val	CAA Gln	384
	AAG Lys	GAA Glu 130	TTA Leu	CAA Gln	CAT His	ATC Ile	GTT Val 135	GGA Gly	TCA Ser	CAG Gln	CAC His	ATC Ile 140	AGA Arg	GCA Ala	GAG Glu	AAA Lys	432
50	GCG Ala 145	ATG Met	GTG Val	GAT Asp	GGC Gly	TCA Ser 150	TGG Trp	TTA Leu	GAT Asp	CTG Leu	GCC Ala 155	AAG Lys	AGG Arg	AGC Ser	AAG Lys	CTT Leu 160	480
55	GAA Glu	GCT Ala	CAG Gln	FIU	TTT Phe 165	GCT ( Ala i	CAT His	CTC Leu	Thr	ATT Ile 170	AAT Asn	GCC Ala	ACC Thr	GAC Asp	ATC Ile 175	CCA Pro	528
60	TCT Ser	GGT Gly	ser	CAT His 180	AAA Lys	GTG :	AGT ( Ser )	Leu :	TCC ' Ser : 185	TCT Ser	TGG Trp	TAC Tyr	His	GAT Asp 190	CGG Arg	GGT Gly	576

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	TGG GCC AAG ATC TCC AAC ATG ACT TTT AGC AAT GGA AAA CTA ATA GTT Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val 195 200 205	624
5	AAT CAG GAT GGC TTT TAT TAC CTG TAT GCC AAC ATT TGC TTT CGA CAT Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His 210 215 220	672
10	CAT GAA ACT TCA GGA GAC CTA GCT ACA GAG TAT CTT CAA CTA ATG GTG His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val 225 230 235 240	720
15	TAC GTC ACT AAA ACC AGC ATC AAA ATC CCA AGT TCT CAT ACC CTG ATG Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met 245 250 255	768
20	AAA GGA GGA AGC ACC AAG TAT TGG TCA GGG AAT TCT GAA TTC CAT TTT Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe 260 265 270	816
	TAT TCC ATA AAC GTT GGT GGA TTT TTT AAG TTA CGG TCT GGA GAG GAA Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu 275 280 285	864
25	ATC AGC ATC GAG GTC TCC AAC CCC TCC TTA CTG GAT CCG GAT CAG GAT Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp 290 295 300	912
30	GCA ACA TAC TITE CCC CCT TITE AND CTT	954
35	(2) INFORMATION FOR SEQ ID NO:13:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 317 amino acids  (B) TYPE: amino acid	
40	(D) TOPOLOGY: linear  (ii) MOLECULE TYPE: protein	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:  Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu  1 5 10 15	
50	Glu Met Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala 20 25 30	
	Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met 35 40 45	
55	Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val 50 55 60	
60	Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser 65 70 75 80  Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn	
	85 90 95	

	Ala	Asp	Phe	Gln 100	Asp	Thr	Thr	Leu	Glu 105	Ser	Gln	Asp	Thr	Lys 110	Leu	Ile
5	Pro	Asp	Ser 115	Cys	Arg	Arg	Ile	Lys 120	Gln	Ala	Phe	Gln	Gly 125	Ala	Val	Gln
10	Lys	Glu 130	Leu	Gln	His	Ile	Val 135	Gly	Ser	Gln	His	Ile 140	Arg	Ala	Glu	Lys
	Ala 145	Met	Val	Asp	Gly	Ser 150	Trp	Leu	Asp	Leu	Ala 155	Lys	Arg	Ser	Lys	Leu 160

- Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro 15 165 170
  - Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly 185
- Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val 20
  - Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His 215
  - His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
- Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met 30 245
  - Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe 265
- 35 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu 275 285
- Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp 295 40
  - Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp 315

45

- (2) INFORMATION FOR SEQ ID NO:14:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1878 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA 55
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
- 60 (vi) ORIGINAL SOURCE: (A) ORGANISM: Murine

- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: Murine Fetal Liver Epithelium
  - (B) CLONE: muRANK
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..1875

5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
- ATG GCC CCG CGC GCC CGG CGG CGC CAG CTG CCC GCG CCG CTG CTG

  Met Ala Pro Arg Ala Arg Arg Arg Gln Leu Pro Ala Pro Leu Leu

  15

  1 5 10 15
- GCG CTC TGC GTG CTC GTT CCA CTG CAG GTG ACT CTC CAG GTC ACT
  Ala Leu Cys Val Leu Leu Val Pro Leu Gln Val Thr
  20 25 30
- CCT CCA TGC ACC CAG GAG AGG CAT TAT GAG CAT CTC GGA CGG TGT TGC 144
  Pro Pro Cys Thr Glu Arg His Tyr Glu His Leu Gly Arg Cys Cys
  35 40 45
- 25 AGC AGA TGC GAA CCA GGA AAG TAC CTG TCC TCT AAG TGC ACT CCT ACC 192
  Ser Arg Cys Glu Pro Gly Lys Tyr Leu Ser Ser Lys Cys Thr Pro Thr
  50 55 60
- TCC GAC AGT GTG TGT CTG CCC TGT GGC CCC GAT GAG TAC TTG GAC ACC 240

  Ser Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Thr

  65 70 75 80
- TGG AAT GAA GAA GAT AAA TGC TTG CTG CAT AAA GTC TGT GAT GCA GGC 288
  Trp Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Ala Gly
  85
  - AAG GCC CTG GTG GCG GTG GAT CCT GGC AAC CAC ACG GCC CCG CGT CGC 336
    Lys Ala Leu Val Ala Val Asp Pro Gly Asn His Thr Ala Pro Arg Arg
    100 105
    - TGT GCT TGC ACG GCT GGC TAC CAC TGG AAC TCA GAC TGC GAG TGC TGC Cys Ala Cys Thr Ala Gly Tyr His Trp Asn Ser Asp Cys Glu Cys Cys 115
- 45 CGC AGG AAC ACG GAG TGT GCA CCT GGC TTC GGA GCT CAG CAT CCC TTG 432
  Arg Arg Asn Thr Glu Cys Ala Pro Gly Phe Gly Ala Gln His Pro Leu
  130 140
- CAG CTC AAC AAG GAT ACG GTG TGC ACA CCC TGC CTC GGC TTC TTC 480
  Gln Leu Asn Lys Asp Thr Val Cys Thr Pro Cys Leu Leu Gly Phe Phe
  145 150 160
- TCA GAT GTC TTT TCG TCC ACA GAC AAA TGC AAA CCT TGG ACC AAC TGC 528

  Ser Asp Val Phe Ser Ser Thr Asp Lys Cys Lys Pro Trp Thr Asn Cys

  165
  - ACC CTC CTT GGA AAG CTA GAA GCA CAC CAG GGG ACA ACG GAA TCA GAT 576
    Thr Leu Leu Gly Lys Leu Glu Ala His Gln Gly Thr Thr Glu Ser Asp
    180 185 190

	IMMUNEX CORPORATION  GTG GTC TGC AGC TCT TCC ATG ACA CTG AGG AGA CCA CCC AAG GAG GCC 6														t No. 2052 A		
	GTG	GTC	TGC	C AGO S Sei	TCI	TCC	ATC	ACA Thi 200	Lei	G AGG	G AG	A CC	A CC0 0 Pro 20	o Ly:	G GAG	G GCC Ala	624
5	CAG Gln	GCT Ala 210	Туг	CTC Leu	CCC Pro	AGT Ser	CTC Leu 215	Ile	GTT Val	r CT( l Lei	G CTO	C CTG Let 220	u Phe	C ATO	C TC'	r GTG c Val	672
10	GTA Val 225	Val	GTC Val	GCT Ala	GCC Ala	11e	: Ile	TTC Phe	GGC Gly	C GTT / Val	TAC Tyr 235	Ty:	C AGO	G AA( g Lys	G GG/ G Gly	A GGG Gly 240	720
15	AAA Lys	GCG Ala	CTG Leu	ACA Thr	GCT Ala 245	Asn	TTG Leu	TGC Trp	AAT Asn	TGC Trp 250	Val	AA? Asr	r GAT n Asr	r GCT o Ala	TGC Cys 255	AGT Ser	768
20	AGT Ser	CTA Leu	AGT Ser	GGA Gly 260	Asn	AAG Lys	GAG Glu	TCC Ser	TCA Ser 265	Gly	GAC Asp	CGT Arg	TG1 JCys	GCT Ala 270	Gly	TCC Ser	816
	CAC His	TCG Ser	GCA Ala 275	Thr	TCC Ser	AGT Ser	CAG Gln	CAA Gln 280	Glu	GTG Val	TGT Cys	GAA Glu	GGT Gly 285	' Iļe	TTA Leu	CTA Leu	864
25	ATG Met	ACT Thr 290	CGG Arg	GAG Glu	GAG Glu	AAG Lys	ATG Met 295	GTT Val	CCA Pro	GAA Glu	GAC Asp	GGT Gly 300	Ala	GGA Gly	GTC Val	TGT Cys	912
30	GGG Gly 305	CCT Pro	GTG Val	TGT Cys	GCG Ala	GCA Ala 310	GGT Gly	GGG Gly	CCC Pro	TGG Trp	GCA Ala 315	GAA Glu	GTC Val	AGA Arg	GAT Asp	TCT Ser 320	960
35	AGG Arg	ACG Thr	TTC Phe	ACA Thr	CTG Leu 325	GTC Val	AGC Ser	GAG Glu	GTT Val	GAG Glu 330	ACG Thr	CAA Gln	GGA Gly	GAC Asp	CTC Leu 335	TCG Ser	1008
40	AGG Arg	AAG Lys	ATT Ile	CCC Pro 340	ACA Thr	GAG Glu	GAT Asp	GAG Glu	TAC Tyr 345	ACG Thr	GAC Asp	CGG Arg	CCC Pro	TCG Ser 350	CAG Gln	CCT Pro	1056
	TCG Ser	ACT Thr	GGT Gly 355	TCA Ser	CTG Leu	CTC Leu	CTA Leu	ATC Ile 360	CAG Gln	CAG Gln	GGA Gly	AGC Ser	AAA Lys 365	TCT Ser	ATA Ile	CCC Pro	1104
45	CCA Pro	TTC Phe 370	CAG Gln	GAG Glu	CCC Pro	CTG Leu	GAA Glu 375	GTG Val	GGG Gly	GAG Glu	AAC Asn	GAC Asp 380	AGT Ser	TTA Leu	AGC Ser	CAG Gln	1152
50	TGT Cys 385	TTC Phe	ACC Thr	GGG Gly	ACT Thr	GAA Glu 390	AGC Ser	ACG Thr	GTG Val	GAT Asp	TCT Ser 395	GAG Glu	GGC Gly	TGT Cys	GAC Asp	TTC Phe 400	1200
55	ACT Thr	GLu	Pro	Pro	Ser 405	Arg	Thr	Asp	Ser	Met 410	Pro	Val	Ser	Pro	Glu 415	Lys	1248
60	CAC His	CTG Leu	ACA Thr	AAA Lys 420	GAA Glu	ATA Ile	GAA Glu	Gly	GAC Asp 425	AGT Ser	TGC Cys	CTC Leu	CCC Pro	TGG Trp 430	GTG Val	GTC Val	1296

	IM	MUN	EX CO	RPO	RATIO	N										Docke	et No. 2852-A
	AG0 Se1	C TC	C AAG r Asr 435	ı ser	A ACA	A GAT	r GGC O Gly	TAC Ty:	r Thi	A GGG	C AG1	r GGC	G AAC / Asr 449	Thi	r cc:	r GGG o Gly	1244
5	GA(	G GAG 1 Ası 450	) His	GAA Glu	CCC Pro	TTT Phe	CCA Pro 455	Gly	G TC( / Sei	C CTC	AAA Lys	TGT Cys 460	Gly	CCA Pro	TT(	G CCC	1392
10	CAC Glr 465	Cys	GCC Ala	TAC Tyr	AGC Ser	Met 470	: Gly	TTT Phe	CCC Pro	AGT Ser	GAA Glu 475	Ala	GCA Ala	GCC Ala	AGC Ser	ATG Met 480	1440
15	GCA Ala	GAC Glu	GCG Ala	GGA Gly	GTA Val 485	Arg	CCC Pro	CAC Glr	GAC Asp	AGG Arg 490	Ala	GAT Asp	GAG Glu	AGG Arg	GGA Gly 495	GCC Ala	1488
20	ser	GIŽ	ser	500	Ser	Ser	Pro	Ser	Asp 505	Gln	Pro	Pro	Ala	Ser 510	Gly	AAC Asn	1536
	GTG Val	ACT Thr	GGA Gly 515	AAC Asn	AGT Ser	AAC Asn	TCC Ser	ACG Thr 520	Phe	ATC Ile	TCT Ser	AGC Ser	GGG Gly 525	CAG Gln	GTG Val	ATG Met	1584
25	AAC Asn	TTC Phe 530	гÀг	GGT Gly	GAC Asp	ATC Ile	ATC Ile 535	GTG Val	GTG Val	TAT Tyr	GTC Val	AGC Ser 540	CAG Gln	ACC Thr	TCG Ser	CAG Gln	1632
30	GAG Glu 545	GGC Gly	CCG Pro	GGT Gly	TCC Ser	GCA Ala 550	GAG Glu	CCC Pro	GAG Glu	TCG Ser	GAG Glu 555	CCC Pro	GTG Val	GGC Gly	CGC Arg	CCT Pro 560	1680
35	GTG Val	CAG Gln	GAG Glu	GAG Glu	ACG Thr 565	CTG Leu	GCA Ala	CAC His	AGA Arg	GAC Asp 570	TCC Ser	TTT Phe	GCG Ala	GGC Gly	ACC Thr 575	GCG Ala	1728
40	CCG Pro	CGC Arg	TTC Phe	CCC Pro 580	GAC Asp	GTC Val	TGT Cys	GCC Ala	ACC Thr 585	GGG Gly	GCT Ala	GGG Gly	CTG Leu	CAG Gln 590	GAG Glu	CAG Gln	1776
	GGG Gly	GCA Ala	CCC Pro 595	CGG Arg	CAG Gln	AAG Lys	GAC Asp	GGG Gly 600	ACA Thr	TCG Ser	CGG Arg	CCG Pro	GTG Val 605	CAG Gln	GAG Glu	CAG Gln	1824
45	GGT Gly	GGG Gly 610	GCG Ala	CAG Gln	ACT Thr	TCA Ser	CTC Leu 615	CAT His	ACC Thr	CAG Gln	Gly	TCC Ser 620	GGA (	CAA Gln	TGT Cys	GCA Ala	1872
50	GAA Glu 625	TGA															1878
55	(2)		-				ID NO										
60				(A) (B) (D)	TYPE TOPO	GTH: E: ai DLOG	625 mino Y: 1:	ami: acid inea:	no a d r	cids							



# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

5	Me	t Al 1	a Pr	o Ar	g Alá	a Arg	g Ar	g Ar	g Ar	g Gl 1		u Pr	o Al	a Pr	o Le	u Leu 5
	Al	a Le	и Су	s Va 2	l Leu 0	ı Leı	ı Va	l Pr	o Le 2	u G1 5	n Va	1 Th	r Le	u Gli		l Thr
10	Pro	o Pr	о Су 3	s Thi	r Glr	ı Glı	ı Arç	g Hi:	s Ту: О	r Gl	u Hi:	s Lei	4 Gly		g Cy:	s Cys
15	Se	r Ar 5	g Су 0	s Gl	ı Pro	Gly	/ Lys	з Тул 5	r Lei	u Se:	r Sei	r Lys		s Thi	r Pro	Thr
	Ser 65	r As	p Se:	r Val	l Cys	Leu 70	Pro	суз	s Gly	y Pro	Ası 75		а Туг	Let	ı Asp	Thr 80
20	Trp	) Ası	n Glı	ı Glu	a Asp 85	Lys	Cys	: Lei	ı Let	His 90		Val	. Суз	asp	95	Gly
	Lys	s Ala	a Lei	1 Val	. Ala	Val	Asp	Pro	Gly 105	/ Asr	His	Thr	Ala	Pro 110		Arg
25	Суз	a Ala	115	Thr	Ala	Gly	Tyr	His 120	Trp	Asn	Ser	Asp	Cys 125		Cys	Cys
30	Arg	130	Asr	Thr	Glu	Суѕ	Ala 135	Pro	Gly	Phe	Gly	Ala 140		His	Pro	Leu
	Gln 145	Leu	ı Asn	Lys	Asp	Thr 150	Val	Cys	Thr	Pro	Cys 155	Leu	Leu	Gly	Phe	Phe 160
35	Ser	Asp	Val	Phe	Ser 165	Ser	Thr	Asp	Lys	Cys 170	Lys	Pro	Trp	Thr	Asn 175	Cys
	Thr	Leu	Leu	Gly 180	Lys	Leu	Glu	Ala	His 185	Gln	Gly	Thr	Thr	Glu 190	Ser	Asp
40	Val	Val	Cys 195	Ser	Ser	Ser	Met	Thr 200	Leu	Arg	Arg	Pro	Pro 205	Lys	Glu	Ala
45		210			Pro		215					220				
	-					230					235					240
50					Ala 245					250					255	
5.5				200	Asn				265					270		
55			275		Ser			280					285			
60	Met	Thr 290	Arg	Glu	Glu 1	Lys 1	Met 295	Val	Pro	Glu		Gly 300	Ala	Gly	Val	Cys

	IM	IMU	NEX	K CC	DRPO	RATI	ON															
	Gl	y F						a Gl	.y G]	Ly Pi	co I	'rp	Ala	a G1	u Va	al A	ra	Asr	Docket Ser	No. 2	852-7	4
	30	15					31	.0				-	315	5			- 9	11.56	320			
5						32	5				3	30						335				
	Ar	g L	ys	Il∈	9 Pro	> Th	r Gl	u As	p Gl	u Ty 34	rT 15	hr	Asp	Ar	g Pr		er 50	Gln	Pro			
10				333					36	0					36	5			Pro			
15		J	, 0					37	5					38	0				Gln			
	30.	,					391	J					395						Phe 400			
20						40.	,				43	.0					4	115	Lys			
25					420		ı Ile			42	5					43	0				•	
25			•	133			Asp		44(	)					445	5						
30			•				Phe	455						460								
	400						Met 470					4	175						480			
35						485	Arg				49	0					4	95				
40					300		Ser			505						510	•					
40			,				Asn		520						525							
45							Ile	235						540								
							Ala 550					5	55					Ē	560			
50						303	Leu				570						57	5				
55	Pro Glv			_	,00					585						590						
-	Gly		و ر	, 5					600						605							
60	Gly	610	N.L	.a હ	·ТП ,	IIII ,	ser	Leu : 615	Hls	Thr	Gln	G1		er 20	Gly	Gln	СУ	s A	la			

# IPHRAKSO ... 101300

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Glu 625 5 (2) INFORMATION FOR SEQ ID NO:16: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids (B) TYPE: amino acid 10 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16: 15 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Trp Val Pro 10 Gly Ser Thr Gly 20 20 (2) INFORMATION FOR SEQ ID NO:17: 25 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 5 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear 30 (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17: 35 Asp Tyr Lys Asp Glu (2) INFORMATION FOR SEQ ID NO:18: 40 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 6 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear 45 (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: 50 His His His His His 5 (2) INFORMATION FOR SEQ ID NO:19: 55 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 amino acids

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(B) TYPE: amino acid(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

5	Arg	Met	Lys	Gln	Ile	Glu	Asp	Lys	Ile	Glu	Glu	Ile	Leu	Ser	Lvs	Ile
5	.1				5					10					15	

Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu 20 25 30

10 Arg